Please cancel claims 36-37 without prejudice or disclaimer, and amend claims 1-2, 4, 31-32, and 34-35 as follows:

1. (Currently Amended) A primer design system, comprising:

    means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of genomic DNA nucleotide sequences;

    means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;

    means for designing a plurality of corresponding primer pairs for each of the predicted exons simultaneously by using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons; and

    means for automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.

2. (Currently Amended) The primer design system according to claim 1, further comprising means for selecting a plurality of primer pairs from the designed primer pairs meeting certain selection conditions from the designed primer pairs.

3. (Previously Presented) The primer design system according to claim 2, wherein said selection conditions include at least one of a predetermined base length, a range of GC content and a range of melting temperature Tm.

4. (Currently Amended) The primer design system according to claim 1, further comprising means for evaluating specificity of each primer of a designed primer pair[[s]] by a sequence alignment program.

5-29. (Cancelled)

30. (Previously Presented) A method for designing primers, comprising the steps of:

    selecting at least one genomic DNA nucleotide sequence from a genomic DNA database;

2

predicting a plurality of exons of said selected DNA nucleotide;

designing corresponding primer pairs for the predicted exons simultaneously by using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons; and

automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.

31.   (Currently Amended) The method for designing primers according to claim 30, further comprising a step of selecting a plurality of primer pairs meeting certain selection conditions from said plurality of designed primer pairs, wherein said selection conditions include at least one of a predetermined base length, a GC content[[,]] and a range of melting temperature Tm.

32.   (Currently Amended) The method for designing primers according to claim 30, further comprising a step of evaluating specificity of each primer of a designed primer pair[[s]].

33.   (Previously Presented) The primer design system according to claim 1, further comprising means for randomly dividing fragments of a genomic DNA into templates for exon prediction.

34.   (Currently Amended) A primer design system, comprising:

means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of genomic DNA nucleotide sequences;

means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;

means for designing a plurality of corresponding primer pairs for each of the predicted exons simultaneously by using each of the predicted exons as a template to design one corresponding primer pair for each of the predicted exons; and

means for evaluating specificity of each primer of designed primer pairs.

35.   (Currently Amended) The primer design system according to claim 34, wherein the system is capable of evaluating each designed primer by conducting homology searches

3

with a certain degree of specificity for a full sequence of the primer via at least one repeat database and at least one genome database.

36-37. (Cancelled)